

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:38:30 ; Search time 95 Seconds  
(without alignments)  
1178.804 Million cell updates/sec

Title: US-10-737-251-51  
Perfect score: 63  
Sequence: 1 gagctcttccgaggtggg.....gctattattagaggagcgaa 63

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/8B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/baCkfileseq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	127	3	US-09-635-132-16
2	33.6	53.3	129	2	US-08-189-256A-25
3	33.6	53.3	129	3	US-09-193-853-25
4	33.6	53.3	140	2	US-08-189-256A-19
5	33.6	53.3	140	3	US-09-193-853-19
6	33.6	53.3	150	2	US-08-189-256A-1
7	33.6	53.3	150	3	US-09-193-853-1
8	33.6	53.3	161	2	US-08-189-256A-18
9	33.6	53.3	161	3	US-09-193-853-18
10	33.6	53.3	164	2	US-08-189-256A-26
11	33.6	53.3	164	3	US-09-193-853-26
12	33.6	53.3	165	2	US-08-189-256A-4
13	33.6	53.3	165	3	US-09-193-853-4
14	33.6	53.3	168	2	US-08-189-256A-2
15	33.6	53.3	168	3	US-09-193-853-2
16	33.6	53.3	168	3	US-09-351-123-5
17	33.6	53.3	184	3	US-09-283-419-3
18	33.6	53.3	201	3	US-09-011-336-58
19	33.6	53.3	202	3	US-09-843-324A-1
20	33.6	53.3	244	3	US-09-351-123-6
21	33.6	53.3	244	3	US-09-843-324A-2
22	33.6	53.3	258	2	US-08-189-256A-24
23	33.6	53.3	258	3	US-09-193-853-24
24	33.6	53.3	300	3	US-09-202-316-4

25	33.6	53.3	300	3	US-09-202-316-7	Sequence 7, Appli
c 26	33.6	53.3	1134	2	US-08-189-256A-10	Sequence 10, Appl
c 27	33.6	53.3	1134	3	US-09-193-853-10	Sequence 10, Appl
c 28	33.6	53.3	1143	3	US-09-142-114B-6	Sequence 6, Appli
29	33.6	53.3	1208	2	US-08-189-256A-28	Sequence 28, Appl
30	33.6	53.3	1208	3	US-09-193-853-28	Sequence 28, Appl
31	33.6	53.3	1416	2	US-08-189-256A-27	Sequence 27, Appl
32	33.6	53.3	1416	3	US-09-193-853-27	Sequence 27, Appl
c 33	33.6	53.3	1417	3	US-09-142-114B-7	Sequence 7, Appli
c 34	33.6	53.3	2962	2	US-08-189-256A-3	Sequence 3, Appli
c 35	33.6	53.3	2962	3	US-09-193-853-3	Sequence 3, Appli
c 36	33.6	53.3	6477	3	US-09-936-588-63	Sequence 63, Appl
37	30.4	48.3	369	3	US-09-265-919-10	Sequence 10, Appl
c 38	30.4	48.3	1993	3	US-09-142-114B-5	Sequence 5, Appli
c 39	30.4	48.3	7455	3	US-09-220-557-19	Sequence 19, Appl
c 40	30.4	48.3	7455	3	US-10-219-227-19	Sequence 13, Appl
41	27	42.9	139	2	US-08-217-360-13	Sequence 17, Appl
42	27	42.9	146	2	US-08-217-360-17	Sequence 17, Appl
43	27	42.9	171	2	US-08-217-360-16	Sequence 16, Appl
44	26.6	42.2	133	3	US-09-445-283C-32	Sequence 32, Appl
45	25.6	40.6	185	3	US-09-283-419-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-635-132-16  
; Sequence 16, Application US/09635132  
; Patent No. 6620601  
; GENERAL INFORMATION:  
; APPLICANT: YAMAGUCHI, ISAMU  
; APPLICANT: NAKASHITA, HIDEO  
; APPLICANT: YOSHIOKA, KEIKO  
; APPLICANT: DOI, YOSHIHARU  
; TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED  
; FILE REFERENCE: 081356/0148  
; CURRENT APPLICATION NUMBER: US/09/635,132  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: JP 11-225832  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: JP 11-225839  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 127  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
US-09-635-132-16

Query Match 53.3%; Score 33.6; DB 3; Length 127;  
Best Local Similarity 81.2%; Pred. No. 0.0011;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTACCTGAGGGGCTCCCTAGGCTATTATAGAGGCGCAA 63  
Db 53 GTGGGATTACCTGAGGGGCGAGGATGCTATTATTTCTGGGAGCGAA 100

RESULT 2  
US-08-189-256A-25  
; Sequence 25, Application US/08189256A  
; Patent No. 5877402  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey  
; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Allison, Lori A.  
; APPLICANT: Carrier, Helaine  
; APPLICANT: Kanevski, Ivan

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? COUNTRY: USA
? ZIP: 19103-2307
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/193,853
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/189,256
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/518,763
? FILING DATE: 01-MAY-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Reed, Janet E.
? REGISTRATION NUMBER: 36,252
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 563-4100
? TELEFAX: (215) 563-4044
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 129 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? US-09-193-853-25

Query Match 53.3%; Score 33.6; DB 3; Length 129;
Best Local Similarity 81.2%; Pred. No. 0.0011; 9; Indels 0; Gaps
Matches 39; Conservative 0; Mismatches 9;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
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DB 46 GTGGGATTGACGTGAGGGGGCAGCGATGGCTATATTCTGGGAGCGAA 93
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RESULT 4
US-08-189-256A-19
? Sequence 19, Application US/08189256A
? Patent No. 5877402
? GENERAL INFORMATION:
? APPLICANT: Maliga, Pal
? APPLICANT: Svab, Zora
? APPLICANT: Staub, Jeffrey
? APPLICANT: Zoubenko, Oleg V.
? APPLICANT: Allison, Lori A.
? APPLICANT: Carrier, Helaine
? APPLICANT: Kanevski, Ivan
? TITLE OF INVENTION: DNA Constructs and Methods for Stably
? TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
? TITLE OF INVENTION: Expressing Recombinant Proteins Therein
? NUMBER OF SEQUENCES: 47
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dann, Dorfman, Herrell and Skillman
? STREET: 1601 Market Street Suite 720
? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19103-2307
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/189,256A

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; FILING DATE: 31-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/111,398  
; FILING DATE: 25-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 19:  
; LENGTH: 140 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-189-256A-19

Query Match 53.3%; Score 33.6; DB 2; Length 140;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63  
Db 57 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGGAGCGAA 104

## RESULT 5

US-09-193-853-19  
; Sequence 19, Application US/09193853  
; Patent No. 6388168  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey  
; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Allison, Lori A.  
; APPLICANT: Carer, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; Transforming Plastids of Multicellular Plants and  
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/193,853  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/189,256  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 19:  
; LENGTH: 140 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-09-193-853-19

Query Match 53.3%; Score 33.6; DB 3; Length 140;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63  
Db 57 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGGAGCGAA 104

## RESULT 6

US-08-189-256A-1  
; Sequence 1, Application US/08189256A  
; Patent No. 5877402  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey  
; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Allison, Lori A.  
; APPLICANT: Carer, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; Transforming Plastids of Multicellular Plants and  
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189,256A  
; FILING DATE: 31-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/111,398  
; FILING DATE: 25-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 150 base pairs  
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-189-256A-1

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Query Match 53.3%; Score 33.6; DB 2; Length 150;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCTAGGCTATATTAGAGGGAGCAA 63  
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Db 41 GTGGGATTGACGTGAGGGGGCAGGATGGCTATATTTCTGGGAGGCAA 88  
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RESULT 7  
 US-09-193-853-1  
 ; Sequence 1, Application US/09193853  
 ; Patent No. 6388168  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maliga, Pal  
 ; APPLICANT: Svab, Zora  
 ; APPLICANT: Staub, Jeffrey  
 ; APPLICANT: Zoubenko, Oleg V.  
 ; APPLICANT: Allison, Lori A.  
 ; APPLICANT: Carrier, Helaine  
 ; APPLICANT: Kanevski, Ivan  
 ; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
 ; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
 ; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
 ; NUMBER OF SEQUENCES: 47  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
 ; STREET: 1601 Market Street Suite 720  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103-2307  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/193,853  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/189,256  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/518,763  
 ; FILING DATE: 01-MAY-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Reed, Janet E.  
 ; REGISTRATION NUMBER: 36,252  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 563-4100  
 ; TELEFAX: (215) 563-4044  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 150 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-09-193-853-1

	Matches	39;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;
Qy	16	GTGGGATTACGTGAGGGGGCTCCCTAGCTATTATTAGAGGGAGCGAA	63							
Db	41	GTGGGATTACGTGAGGGGGCAGGGATGGCTATTATTTCTGGAGCGAA	88							

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RESULT 8
US-08-189-256A-18
: Sequence 18, Application US/08189256A
: Patent No. 5877402
: GENERAL INFORMATION:
: APPLICANT: Maliga, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrer, Helaine
: APPLICANT: Kanevski, Ivan
: TITLE OF INVENTION: DNA Constructs and Methods for Stably
: TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
: TITLE OF INVENTION: Expressing Recombinant Proteins Therein
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman
: STREET: 1601 Market Street Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/189,256A
: FILING DATE: 31-JAN-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/111,398
: FILING DATE: 25-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/518,763
: FILING DATE: 01-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4044
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 161 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
US-08-189-256A-18

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QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63  
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Db 63 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTGGGAGCGAA 110  
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RESULT 9  
US-09-193-853-18

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; Sequence 18, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09193,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; NAME: Reed, Janet E.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4044
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-193-853-18

Query Match 53.3%; Score 33.6; DB 3; Length 161;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 63 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 110

RESULT 10
US-08-189-256A-26
; Sequence 26, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
```

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; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; NAME: Reed, Janet E.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4040
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-189-256A-26

Query Match 53.3%; Score 33.6; DB 2; Length 164;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 46 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 93

RESULT 11
US-09-193-853-26
; Sequence 26, Application US/09193853
; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrier, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
```

; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/193,853  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/189,256  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 164 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-193-853-26

Query Match 53.3%; Score 33.6; DB 3; Length 164;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63  
|||||  
DB 46 GTGGGATTGACGTGAGGGGGCGAGGATGCTATATTCTGGGAGCGAA 93  
|||||

RESULT 12  
US-08-189-256A-4  
; Sequence 4, Application US/08189256A  
; Patent No. 5877402  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey  
; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Allison, Lori A.  
; APPLICANT: Carrier, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/189,256A  
; FILING DATE: 31-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/111,398  
; FILING DATE: 25-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 165 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-189-256A-4

Query Match 53.3%; Score 33.6; DB 2; Length 165;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63  
|||||  
DB 41 GTGGGATTGACGTGAGGGGGCGAGGATGCTATATTCTGGGAGCGAA 88  
|||||

RESULT 13  
US-09-193-853-4  
; Sequence 4, Application US/09193853  
; Patent No. 6388168  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey  
; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Allison, Lori A.  
; APPLICANT: Carrier, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/193,853  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/189,256  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-4

Query Match 53.3%; Score 33.6; DB 3; Length 165;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
Db 41 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 88

## RESULT 14

US-08-189-256A-2  
Sequence 2, Application US/08189256A  
Patent No. 5877402  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carrier, Helaine  
APPLICANT: Kanevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
Transforming Plastids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/189,256A  
FILING DATE: 31-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/111,398  
FILING DATE: 25-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-189-256A-2

Query Match 53.3%; Score 33.6; DB 2; Length 168;  
Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
Db 41 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTTGGGAGCGAA 88

## RESULT 15

US-09-193-853-2  
Sequence 2, Application US/09193853  
Patent No. 6388168  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carrier, Helaine  
APPLICANT: Kanevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
Transforming Plastids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/193,853  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,256  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518,763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-2

Query Match

53.3%; Score 33.6; DB 3; Length 168;

Best Local Similarity 81.2%; Pred. No. 0.0012;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
|||  
Db 41 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTGGGAGCGAA 88  
|||

Search completed: February 21, 2006, 05:40:12  
Job time : 95 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:41:51 ; Search time 410 Seconds  
(without alignments)  
326.188 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttcctcgagtgagg.....gctattattagaggagcgaa 63

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications NA New:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	33.6	53.3	2569	9	US-11-190-122-3
3	33.6	53.3	2800	9	US-11-190-122-1
4	33.6	53.3	3119	9	US-11-190-122-2
5	33.6	53.3	5834	7	US-10-527-048-15
6	33.6	53.3	6465	7	US-10-527-048-25
7	33.6	53.3	6659	7	US-10-527-048-22
8	33.6	53.3	7549	7	US-10-527-048-24
9	25.6	40.6	562	6	US-09-925-065A-935299
10	25.6	40.6	562	6	US-09-925-065A-935300
11	25.6	40.6	562	6	US-09-925-065A-952905
12	25.6	40.6	562	6	US-09-925-065A-952906
13	25.6	40.6	624	6	US-09-925-065A-952906
14	25.6	40.6	56054	8	US-10-995-561-13402
15	24.2	38.4	561	6	US-09-925-065A-753058
16	24.2	38.4	561	6	US-09-925-065A-824463
17	24.2	38.4	594	6	US-09-925-065A-308387
18	24.2	38.4	594	6	US-09-925-065A-308388
19	24.2	38.4	594	6	US-09-925-065A-308389
20	24.2	38.4	615	6	US-09-925-065A-753057

Sequence 824462,	615	6	US-09-925-065A-824462	21	24.2	38.4	2136	6	US-09-925-065A-705163
Sequence 1716, Ap	2136	9	US-11-072-512-1716	22	24.2	38.4	2136	9	US-11-072-512-1716
Sequence 513697,	537	6	US-09-925-065A-513697	23	24	38.1	537	6	US-09-925-065A-513697
Sequence 926199,	607	6	US-09-925-065A-926199	24	24	38.1	607	6	US-09-925-065A-926199
Sequence 948723,	607	6	US-09-925-065A-948723	25	24	38.1	607	6	US-09-925-065A-948723
Sequence 539618,	608	6	US-09-925-065A-539618	26	23.8	37.8	608	6	US-09-925-065A-539618
Sequence 539617,	608	6	US-09-925-065A-539617	27	23.8	37.8	608	6	US-09-925-065A-539617
Sequence 519220,	629	6	US-09-925-065A-519220	28	23.8	37.8	629	6	US-09-925-065A-519220
Sequence 36107, A	2034	6	US-09-925-065A-36107	29	23.8	37.8	2034	6	US-09-925-065A-36107
Sequence 40864, A	2102	6	US-09-925-065A-40864	30	23.8	37.8	2102	6	US-09-925-065A-40864
Sequence 40865, A	2102	6	US-09-925-065A-40865	31	23.8	37.8	2102	6	US-09-925-065A-40865
Sequence 725519,	2644	6	US-09-925-065A-725519	32	23.8	37.8	2644	6	US-09-925-065A-725519
Sequence 587132,	431	6	US-09-925-065A-587132	33	23.6	37.5	431	6	US-09-925-065A-587132
Sequence 67485, A	642	6	US-09-925-065A-67485	34	23.6	37.5	642	6	US-09-925-065A-67485
Sequence 67486, A	642	6	US-09-925-065A-67486	35	23.6	37.5	642	6	US-09-925-065A-67486
Sequence 231, App	586	6	US-09-925-065A-231	36	23.4	37.1	586	6	US-09-925-065A-231
Sequence 864288,	645	6	US-09-925-065A-864288	37	23.4	37.1	645	6	US-09-925-065A-864288
Sequence 36, Appl	98345	12	US-11-112-908-36	38	23.4	37.1	98345	12	US-11-112-908-36
Sequence 86646, A	1462	6	US-09-925-065A-86646	39	23.2	36.8	1462	6	US-09-925-065A-86646
Sequence 86647, A	1462	6	US-09-925-065A-86647	40	23.2	36.8	1462	6	US-09-925-065A-86647
Sequence 86648, A	1462	6	US-09-925-065A-86648	41	23.2	36.8	1462	6	US-09-925-065A-86648
Sequence 831, App	2424	8	US-10-909-125-831	42	23.2	36.8	2424	8	US-10-909-125-831
Sequence 66, Appl	163162	12	US-11-121-086-66	43	23.2	36.8	163162	12	US-11-121-086-66
Sequence 783808,	591	6	US-09-925-065A-783808	44	23	36.5	591	6	US-09-925-065A-783808
Sequence 705163,	2136	6	US-09-925-065A-705163	45	23	36.5	2136	6	US-09-925-065A-705163

#### ALIGNMENTS

#### RESULT 1

US-10-527-048-14

; Sequence 14, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 176

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

; OTHER INFORMATION: fragment codifying for the promoter region of the plastid 16S

; OTHER INFORMATION: ribosomal RNA (Prn), with added restriction sites.

US-10-527-048-14

Query Match 53.3%; Score 33.6; DB 7; Length 176;

Best Local Similarity 81.2%; Pred. No. 0.0028;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 56 GTGGGATTGACCTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 103

#### RESULT 2

US-11-190-123-3

; Sequence 3, Application US/11190122

; Publication No. US20060031964A1

; GENERAL INFORMATION:

; APPLICANT: Daniell, Henry

; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis

; FILE REFERENCE: CHL-T107C322

; CURRENT APPLICATION NUMBER: US/11/190,122

; CURRENT FILING DATE: 2005-07-25

; PRIOR APPLICATION NUMBER: 60/344,704

; PRIOR FILING DATE: 2001-12-26

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; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: pct/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: apha-6/nptII expression cassette
US-11-190-122-3

Query Match      53.3%; Score 33.6; DB 9; Length 2569;
Best Local Similarity 81.2%; Pred. No. 0.004;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGAGCGAA 63
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DB      119 GTGGGATTGACGTGAGGGGCGCAGGATGGCTATATTCTTGGAGCGAA 166
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RESULT 3
US-11-190-122-1
; Sequence 1, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: pct/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: ARTIFICIAL
```

```
; FEATURE:
; OTHER INFORMATION: aadA/BADH expression cassette
US-11-190-122-1

Query Match      53.3%; Score 33.6; DB 9; Length 2800;
Best Local Similarity 81.2%; Pred. No. 0.004;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGAGCGAA 63
      |||||||
DB      125 GTGGGATTGACGTGAGGGGCGCAGGATGGCTATATTCTTGGAGCGAA 172

RESULT 4
US-11-190-122-2
; Sequence 2, Application US/11190122
; Publication No. US20060031964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHL-T107C322
; CURRENT APPLICATION NUMBER: US/11/190,122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 10/500,351
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: pct/us2003/021157
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/590,848
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/590,751
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 10/519,821
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/400,816
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/393,651
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/393,428
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: pct/US2002/041503
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 3119
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: gfp/BADH expression cassette
US-11-190-122-2

Query Match      53.3%; Score 33.6; DB 9; Length 3119;
Best Local Similarity 81.2%; Pred. No. 0.0041;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGGAGCGAA 63
      |||||||
DB      119 GTGGGATTGACGTGAGGGGCGCAGGATGGCTATATTCTTGGAGCGAA 166

RESULT 5
US-10-527-048-15
; Sequence 15, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/527,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 5834

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
; OTHER INFORMATION: fragment from the vector pVTPA between the rice atpB and  
; OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-15

Query Match 53.3%; Score 33.6; DB 7; Length 5834;

Best Local Similarity 81.2%; Pred. No. 0.0044;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 2005

RESULT 6

US-10-527-048-25

; Sequence 25, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 6465

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
; OTHER INFORMATION: fragment from the vector pVTPA-Bar between the rice atpB and  
; OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-25

Query Match 53.3%; Score 33.6; DB 7; Length 6465;

Best Local Similarity 81.2%; Pred. No. 0.0044;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 2005

RESULT 7

US-10-527-048-22

; Sequence 22, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 6659

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
; OTHER INFORMATION: fragment from the vector pVTPA-aada between the rice atpB and  
; OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-22

Query Match 53.3%; Score 33.6; DB 7; Length 6659;

Best Local Similarity 81.2%; Pred. No. 0.0045;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 1958 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 2005

RESULT 8

US-10-527-048-24

; Sequence 24, Application US/10527048

; Publication No. US20060026704A1

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology.

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 7549

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DN.  
; OTHER INFORMATION: fragment from the vector pVTPA-HB-aada between the rice atpB .  
; OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 7549;

Best Local Similarity 81.2%; Pred. No. 0.0045;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63

Db 2848 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 2895

RESULT 9

US-09-925-065A-935299

; Sequence 935299, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 935299

; LENGTH: 562

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-935299

Query Match 40.6%; Score 25.6; DB 6; Length 562;

Best Local Similarity 66.1%; Pred. No. 3.5;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;



## US-09-925-065A-693983

Query Match 40.6%; Score 25.6; DB 6; Length 624;  
Best Local Similarity 66.1%; Pred. No. 3.5;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGG 56  
|||||  
Db 445 GAGCCCTTCTCCGGGCTGGCTGAGGCTGAGCGGGCTCCCTCGGCTTGTGGGGAGG 500  
|||||

## RESULT 14

US-10-995-561-13402  
; Sequence 13402, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13402  
; LENGTH: 56054  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(56054)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-995-561-13402

Query Match 40.6%; Score 25.6; DB 8; Length 56054;  
Best Local Similarity 66.1%; Pred. No. 6.2;  
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGG 56  
|||||  
Db 5170 GAGCCCTTCTCTGGGCTGGCTAGTCCGAGCGGGCTCCCTCGGCTTGTGGGGAGG 5225  
|||||

## RESULT 15

US-09-925-065A-753058  
; Sequence 753058, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 753058  
; LENGTH: 561  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-753058

Query Match 38.4%; Score 24.2; DB 6; Length 561;  
Best Local Similarity 66.0%; Pred. No. 12;  
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAG 53  
|||||  
Db 254 GAGCCCTTCTCTGGGCTGGCGGAGGCTGAGCCGGCTCCCTCAGCTTGGTTTG 306  
|||||

Search completed: February 21, 2006, 06:33:19  
Job time : 411 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:40:29 ; Search time 492 Seconds  
(without alignments)  
1058.884 Million cell updates/sec

Title: US-10-737-251-51  
Perfect score: 63  
Sequence: 1 gagctctctccagggtggg.....gctatataggaggagcgaa 63

Scoring table: IDENTITY NUC  
Gapop 10^0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
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6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	8	US-10-737-251-51
2	38.4	61.0	112	8	US-10-737-251-18
3	38.4	61.0	112	8	US-10-737-251-19
4	38.4	61.0	112	8	US-10-737-251-23
5	36.6	58.1	112	8	US-10-737-251-10
6	34.8	55.2	112	8	US-10-737-251-9
7	33.6	53.3	112	8	US-10-737-251-3
8	33.6	53.3	112	8	US-10-737-251-4
9	33.6	53.3	112	8	US-10-737-251-5
10	33.6	53.3	112	8	US-10-737-251-6
11	33.6	53.3	112	8	US-10-737-251-7
12	33.6	53.3	112	8	US-10-737-251-8
13	33.6	53.3	112	8	US-10-737-251-27
14	33.6	53.3	112	8	US-10-737-251-28
15	33.6	53.3	112	8	US-10-737-251-29
16	33.6	53.3	112	8	US-10-737-251-30
17	33.6	53.3	119	8	US-10-881-813-6
18	33.6	53.3	202	3	US-09-843-324A-1
19	33.6	53.3	220	7	US-10-095-514-3
20	33.6	53.3	233	8	US-10-737-251-38
21	33.6	53.3	234	8	US-10-737-251-42
22	33.6	53.3	244	3	US-09-843-324A-2
23	33.6	53.3	1143	6	US-10-460-716-2

24	33.6	53.3	1417	6	US-10-460-716-3	Sequence 3, Appli	
C	25	33.6	1544	7	US-10-473-207-4	Sequence 4, Appli	
26	33.6	53.3	2145	7	US-10-473-207-26	Sequence 26, Appl	
27	33.6	53.3	2391	7	US-10-473-207-25	Sequence 25, Appl	
C	28	33.6	6477	7	US-10-377-134-63	Sequence 63, Appl	
C	29	33.6	7652	7	US-10-680-824A-1	Sequence 1, Appli	
30	33.6	53.3	8684	7	US-10-680-824A-2	Sequence 2, Appli	
C	31	33.6	8684	7	US-10-680-824A-2	Sequence 2, Appli	
32	33.6	53.3	10011	7	US-10-680-824A-19	Sequence 19, Appl	
33	33.6	53.3	10011	9	US-10-957-562-4	Sequence 4, Appli	
34	32.6	51.7	179	8	US-10-737-251-1	Sequence 1, Appli	
35	32	50.8	233	8	US-10-737-251-41	Sequence 41, Appl	
36	30.6	48.6	112	8	US-10-737-251-11	Sequence 11, Appl	
37	30.6	48.6	112	8	US-10-737-251-26	Sequence 26, Appl	
38	30.6	48.6	130	5	US-10-109-812-1	Sequence 1, Appli	
39	30.6	48.6	131	5	US-10-109-812-4	Sequence 4, Appli	
40	30.4	48.3	183	6	US-10-258-253-16	Sequence 16, Appl	
41	30.4	48.3	237	8	US-10-737-251-43	Sequence 43, Appl	
C	42	30.4	48.3	1993	6	US-10-460-716-1	Sequence 1, Appli
C	43	30.4	48.3	4586	6	US-10-460-716-4	Sequence 4, Appli
C	44	30.4	48.3	7455	5	US-10-219-227-19	Sequence 19, Appl
45	29.6	47.0	1049	5	US-10-109-812-13	Sequence 13, Appl	

## ALIGNMENTS

RESULT 1  
US-10-737-251-51  
; Sequence 51, Application US/10737251  
; Publication No. US20040221338A1  
; GENERAL INFORMATION:  
; APPLICANT: Pal Maliga  
; APPLICANT: Jon Y. Suzuki  
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for  
; FILE REFERENCE: Construction of Chimeric Promoters for Transgene Expression  
; CURRENT APPLICATION NUMBER: US/10737,251  
; CURRENT FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: 60/433,302  
; PRIOR FILING DATE: 2002-12-13  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 51  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutant Prmn  
US-10-737-251-51

Query Match 100.0%; Score 63; DB 8; Length 63;  
Best Local Similarity 100.0%; Pred. No. 2.6e-15;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGC 60  
|||  
Db 1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGC 60

QY 61 GAA 63  
|||  
Db 61 GAA 63

## RESULT 2

US-10-737-251-18  
; Sequence 18, Application US/10737251  
; Publication No. US20040221338A1  
; GENERAL INFORMATION:  
; APPLICANT: Pal Maliga  
; APPLICANT: Jon Y. Suzuki  
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for  
; Transgene Expression

```
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-18

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCTCCGATGGCTATATTCTGGGAGCGAA 75

RESULT 3
US-10-737-251-19
; Sequence 19, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-19

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCTCCGATGGCTATATTCTGGGAGCGAA 75

RESULT 4
US-10-737-251-23
; Sequence 23, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 23
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-23

Query Match      61.0%; Score 38.4; DB 8; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.2e-05;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCTCCGATGGCTATATTAGAGGAGCGAA 75

RESULT 5
US-10-737-251-10
; Sequence 10, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-10

Query Match      58.1%; Score 36.6; DB 8; Length 112;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 13 GAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 25 GAGGTGGGATTGACGTGAGGGGCTCCGATGGCTATATTCTGGGAGCGAA 75

RESULT 6
US-10-737-251-9
; Sequence 9, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-9
```

```
Query Match      55.2%; Score 34.8; DB 8; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.00064;
Matches 42; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 10 TCCGAGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 22 TCCCTCGTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 7
US-10-737-251-3
; Sequence 3, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-3

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 8
US-10-737-251-4
; Sequence 4, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-4

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 11
US-10-737-251-7
; Sequence 7, Application US/10737251
; Publication No. US20040221338A1
```

```
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 9
US-10-737-251-5
; Sequence 5, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-5

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 10
US-10-737-251-6
; Sequence 6, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-6

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 11
US-10-737-251-7
; Sequence 7, Application US/10737251
; Publication No. US20040221338A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-7

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 12
US-10-737-251-8
; Sequence 8, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-8

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 13
US-10-737-251-27
; Sequence 27, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
```

```
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-27

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 14
US-10-737-251-28
; Sequence 28, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prn promoter derivative
US-10-737-251-28

Query Match          53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 28 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 75

RESULT 15
US-10-737-251-29
; Sequence 29, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 112
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prm promoter derivative
US-10-737-251-29

Query Match      53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGCGCAA 63
        |||||
Db      28 GTGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGCGCAA 75

Search completed: February 21, 2006, 05:48:49
Job time : 493 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:37:59 ; Search time 3773 Seconds  
(without alignments)  
781.231 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctctctccagggtggg.....gctatattaggaggcgaa 63

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

```
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hrc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32	50.8	243	9	BH009665 ef31f05.x
2	32	50.8	295	9	BZ457960 BOND72TR
3	32	50.8	380	7	CN859023 000728AAA
4	32	50.8	395	9	BH678911 BOMDD83TR
5	32	50.8	415	7	CN930271 000322AFB
6	32	50.8	498	7	CN872595 020807AAP
C 7	32	50.8	510	1	AJ876197 AJ876197
8	32	50.8	561	9	BH522564 BQGRW45TF
9	32	50.8	598	7	CN871707 010128AAP
C 10	32	50.8	734	10	CG026772 PGAAE374TR
C 11	32	50.8	764	10	CG026604 PGAAE30TF
12	32	50.8	825	9	BZ498361 BONLE43TF
C 13	30.4	48.3	169	9	AQ962940 LERGI42TR
C 14	30.4	48.3	183	9	BZ483881 BOAI129TR
C 15	30.4	48.3	194	9	AQ962945 LERGI45TR
16	30.4	48.3	199	9	BH537952 BOGFU38TR
17	30.4	48.3	238	9	BH677595 BOMCMA9TR
18	30.4	48.3	244	9	BH588286 BOGFU54TF
19	30.4	48.3	292	9	BH474703 BOCQI49TF
20	30.4	48.3	299	9	BZ507339 BOPU16TF
21	30.4	48.3	305	8	DT034079 VIL089A04
C 22	30.4	48.3	305	9	BH646726 BQGRW48TF

23	30.4	48.3	322	9	BH705426
24	30.4	48.3	326	9	BZ440851
25	30.4	48.3	337	9	BZ440851
26	30.4	48.3	344	9	BZ476987
27	30.4	48.3	361	9	BZ470963
28	30.4	48.3	364	9	BH558977
29	30.4	48.3	367	9	BH430502
30	30.4	48.3	368	9	BH493122
31	30.4	48.3	396	9	BH630640
32	30.4	48.3	405	9	BH427396
33	30.4	48.3	407	9	BZ489878
C 34	30.4	48.3	410	9	BH549701
35	30.4	48.3	416	9	BH664090
36	30.4	48.3	419	9	BH662193
37	30.4	48.3	422	9	BH475597
38	30.4	48.3	423	9	BH653681
39	30.4	48.3	426	9	AQ968706
40	30.4	48.3	434	9	BH545732
41	30.4	48.3	434	9	BH678091
42	30.4	48.3	435	9	BZ447238
43	30.4	48.3	440	9	BH543946
44	30.4	48.3	441	9	BH657205
45	30.4	48.3	441	9	CC966698

#### ALIGNMENTS

RESULT 1  
BH009665/c  
LOCUS ef31f05.x1 TO1000 Brassica oleracea genomic clone ef31f05 5',  
DEFINITION genomic survey sequence.  
ACCESSION BH009665  
VERSION BH009665.1 GI:13955602  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 243)  
AUTHORS Katarai,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J.,  
Baliya,V., Bell,M., Cunnius,D.M., King,L., Kirchoff,K., Kuit,K.,  
Miller,B., Nascimento,L., Preston,R., Rodriguez,S., Santos,L.,  
Shah,R., Vil,M.D., Zutavern,T., Bal,H., Dedhia,N. and McCombie,W.R.  
Whole Genome Shotgun Reads from Brassica oleracea  
Unpublished (2001)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mccombie@cshl.org  
Plate: ef31 row: f column: 05  
Seq primer: -21fwdUniv  
Class: shotgun  
High quality sequence stop: 243.

FEATURES  
source  
1..243  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone="ef31f05"  
/notes="Vector: M13 for .x reads, pzero-2 for .b and .g  
reads; Site 1: EcoRV; DNA prepared as whole genome shotgun  
library from young, green leaves. May contain some plasmid  
DNAs. DNA provided by Dr. Tom Osborn, University of  
Wisconsin-Madison, Department of Agronomy."

ORIGIN

```

Query Match      50.8%; Score 32; DB 9; Length 243;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 97 GTGGGATTGACGTGAGGGGTACGGGTAGCTATATTCTGGGAGCGAA 50
|||||

RESULT 2
BZ457960
LOCUS BOND72TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BOND72,
DEFINITION genomic survey sequence.
ACCESSION BZ457960
VERSION BZ457960.1 GI:26737897
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 295)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..295
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOND72"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site 1: BatXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BatXI linkers"

ORIGIN
Query Match      50.8%; Score 32; DB 9; Length 295;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 199 GTGGGATTGACGTGAGGGGTACGGGTAGCTATATTCTGGGAGCGAA 246
|||||

RESULT 3
CN859023
LOCUS 000728AAAA008805HT (AAAA) Royal Gala 59 DAFB fruit, seeds removed
DEFINITION Malus x domestica cDNA clone AAAA008805, mRNA sequence.
ACCESSION CN859023
VERSION CN859023.1 GI:48114953
KEYWORDS EST.
SOURCE Malus x domestica
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 380)

```

```

AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1..380
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAAA008805"
/tissue_type="fruit"
/dev_stage="59 days after full bloom, seeds removed"
/clone_lib="(AAAA) Royal Gala 59 DAFB fruit, seeds
removed"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN
Query Match      50.8%; Score 32; DB 7; Length 380;
Best Local Similarity 79.2%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
|||||
Db 285 GTGGGATTGACGTGAGGGGTAGGGATGGCTATATTCTGGGAGCGAA 332
|||||

RESULT 4
BH678911
LOCUS BOMDD83TR BO_2_3_KB Brassica oleracea genomic clone BOMDD83,
DEFINITION genomic survey sequence.
ACCESSION BH678911
VERSION BH678911.1 GI:18749354
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 395)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..395
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMDD83"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site 1: BatXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BatXI linkers"

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## ORIGIN

Query Match 50.8%; Score 32; DB 9; Length 395;  
 Best Local Similarity 79.2%; Pred. No. 1.1;  
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 Db 92 GTGGGATTGACGTGAGGGGGTACGGTAGCTATATTCTGGAGCGAA 139  
 |||||

## RESULT 5

CN930271 415 bp mRNA linear EST 07-JUN-2004  
 LOCUS 000322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x  
 DEFINITION domestica cDNA clone AFBC002396, mRNA sequence.

CN930271  
 ACCESSION CN930271  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.

## REFERENCE

AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,  
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave, A.  
 Sequencing Facility  
 The Horticulture and Food Research Institute of New Zealand Ltd  
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

## FEATURES

source  
 1. 415  
 /organism="Malus x domestica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3750"  
 /clone="AFBC002396"  
 /tissue\_type="Floral bud"  
 /dev\_stage="Pre-opening, flower at stage of nectar/pollen  
 formation"  
 /clone\_lib="(AFBC) Royal Gala pre-opened floral bud"  
 /note="Vector: pBK-CMV; Library sequenced by Genesis  
 Research & Development"

## ORIGIN

Query Match 50.8%; Score 32; DB 7; Length 415;  
 Best Local Similarity 79.2%; Pred. No. 1.1;  
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 Db 236 GTGGGATTGACGTGAGGGGGTACGGTAGCTATATTCTGGAGCGAA 283  
 |||||

## RESULT 6

CN872595 498 bp mRNA linear EST 04-JUN-2004  
 LOCUS 020807AAPA005328HT (AAPA) Royal Gala 24 DAFB fruit Malus x  
 DEFINITION domestica cDNA clone AAPA005328, mRNA sequence.

CN872595  
 ACCESSION CN872595  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.  
 1 (bases 1 to 498)

## REFERENCE

## AUTHORS

Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,  
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave, A.  
 Sequencing Facility  
 The Horticulture and Food Research Institute of New Zealand Ltd  
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

## FEATURES

source  
 1. 498  
 /organism="Malus x domestica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3750"  
 /clone="AAPA005328"  
 /tissue\_type="Fruit"  
 /dev\_stage="24 days after full bloom"  
 /clone\_lib="(AAPA) Royal Gala 24 DAFB fruit"  
 /note="Vector: pBK-CMV; Library sequenced by Genesis  
 Research & Development"

## ORIGIN

Query Match 50.8%; Score 32; DB 7; Length 498;  
 Best Local Similarity 79.2%; Pred. No. 1.1;  
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 Db 287 GTGGGATTGACGTGAGGGGGTACGGTAGCTATATTCTGGAGCGAA 334  
 |||||

## RESULT 7

AJ876197/c 510 bp mRNA linear EST 17-FEB-2005  
 LOCUS AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after  
 DEFINITION bloom Prunus persica cDNA clone PR0213A05, mRNA sequence.

ACCESSION AJ876197  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Prunus persica (peach)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 1 (bases 1 to 510)

## REFERENCE

## AUTHORS

Le Dantec, L., Cosson, P., Renaud, C., Garcia, V., Dumoulin, P.,  
 Rothan, C., Filippi, G., Laigret, F., Moing, A. and Dirlewanger, E.  
 Peach (Prunus persica (L.) Batsch) fruit ESTs from two early  
 development stages  
 Unpublished (2004)

## TITLE

## JOURNAL

## COMMENT

## FEATURES

source  
 1. 510  
 /organism="Prunus persica"  
 /mol\_type="mRNA"  
 /cultivar="Fantasia"  
 /db\_xref="taxon:3760"  
 /clone="PR0213A05"  
 /tissue\_type="fruit mesocarp plus epidermis"  
 /dev\_stage="80 days after bloom"  
 /clone\_lib="Prunus persica fruit mesocarp plus epidermis  
 80 days after bloom"

## ORIGIN

Query Match 50.8%; Score 32; DB 1; Length 510;  
 Best Local Similarity 79.2%; Pred. No. 1.1;  
 Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63



Qy 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 Db 114 GTGGATTGACGTGAGGGGCTAGGATGGCTATATTCTGGGAGCGAA 67  
 |||||

## RESULT 11

CG026604/c

LOCUS

DEFINITION PGAAE30TF PGAA Carica papaya genomic clone PGAAE30, genomic survey sequence.

ACCESSION

CG026604

VERSION

CG026604.1

KEYWORDS

SOURCE

ORGANISM

Carica papaya (papaya)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Caricaceae; Carica.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other\_GSSs: PGAAE30TF

Contact: Chris Town

TIGR

7912 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA provided by Ray Ming was isolated from cultivar SunUp that was transgenic for papaya ringspot virus coat protein gene

Seq primer: TF

Class: sheared ends.

FEATURES

source

1..764

/organism="Carica papaya"

/mol\_type="genomic DNA"

/cultivar="SunUp"

/db\_xref="taxon:3649"

/clone\_lib="PGAA"

/note="vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match

Best Local Similarity

Matches

36; Conservative

0; Mismatches

10; Indels

0; Gaps

0;

Qy

Db

16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 622 GTGGATTGACGTGAGGGGCTAGGATGGCTATATTCTGGGAGCGAA 575  
 |||||

RESULT 12

BZ498361

LOCUS

DEFINITION

BZ498361

ACCESSION

BZ498361

VERSION

BZ498361.1

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

TITLE

JOURNAL

Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)

PUBMED

COMMENT

TIGR

Other\_GSSs: BONLE43TR

Contact: Chris Town

7912 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES

source

1..825

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TO1000DH3"

/db\_xref="taxon:3712"

/clones="BONLE43"

/clone\_lib="BO 1.6.2 KB tot"

/note="vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match

Best Local Similarity

Matches

38; Conservative

0; Mismatches

10; Indels

0; Gaps

0;

Qy

Db

16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 4 GTGGATTGACGTGAGGGGTTTGGGTAGCTATATTCTTGGGAGCGAA 51  
 |||||

RESULT 13

AQ962940/c

LOCUS

DEFINITION

AQ962940

ACCESSION

AQ962940

VERSION

AQ962940.1

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: at@tigr.org

For additional information, see http://www.tigr.org/cdb/at/at.html

Similar to A. thaliana chloroplast sequence (GB:AP000423)

Seq primer: TR

Class: shotgun.

FEATURES

source

1..169

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Landsberg erecta"

/db\_xref="taxon:3702"

/clone="LERGI42"

/clone\_lib="LERG"

/notes="Organ: Leaf; Vector: pUC19UK; Total genomic DNA was sheared to 0.4-0.7 kbp before ligation."

ORIGIN

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Query Match      48.3%; Score 30.4; DB 9; Length 169;
Best Local Similarity 77.1%; Pred. No. 3.8;
Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGATTGACCTGAGGGGCTCCCTAGCTATATTAGAGGAGCGAA 63
|||||
Db 118 GTGGATTGACGTGAGGGGTAGGGGTAGCTATATTTCTGGAGCGAA 71
|||||

RESULT 14
BZ483881
LOCUS BZ483881
DEFINITION BOOA129TR BO.1.6.2_KB tot Brassica oleracea genomic clone BOOA129,
genomic survey sequence.
ACCESSION BZ483881
VERSION BZ483881.1 GI:26786279
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 183)
AUTHORS Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, X., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BOOA129TF
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES             Location/Qualifiers
     source           1..183
     organism="Brassica oleracea"
     mol_type="genomic DNA"
     strain="TO1000DH3"
     db_xref="taxon:3712"
     clone_lib="BOOA129"
     clone_lib="BO.1.6.2_KB_tot"
     note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
Query Match      48.3%; Score 30.4; DB 9; Length 183;
Best Local Similarity 77.1%; Pred. No. 3.9;
Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGATTGACCTGAGGGGCTCCCTAGCTATATTAGAGGAGCGAA 63
|||||
Db 62 GTGGATTGACGTGAGGGGTAGGGGTAGCTATATTTCTGGAGCGAA 109
|||||

RESULT 15
AQ962945/c
LOCUS AQ962945/c
DEFINITION LERG145TR LERG Arabidopsis thaliana genomic clone LERG145, genomic
survey sequence.
ACCESSION AQ962945
VERSION AQ962945.1 GI:6790646
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

```

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 194)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Feidblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TR
Class: Shotgun.

FEATURES             Location/Qualifiers
     source           1..194
     organism="Arabidopsis thaliana"
     mol_type="genomic DNA"
     ecotype="Landsberg erecta"
     db_xref="taxon:3702"
     clone_lib="LERG145"
     note="Organ: Leaf; Vector: pUC19UK; Total genomic DNA was
sheared to 0.4-0.7 kbp before ligation."

ORIGIN
Query Match      48.3%; Score 30.4; DB 9; Length 194;
Best Local Similarity 77.1%; Pred. No. 3.9;
Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGCTATATTAGAGGAGCGAA 63
|||||
Db 137 GTGGATTGACGTGAGGGGTAGGGGTAGCTATATTTCTGGAGCGAA 90
|||||

Search completed: February 21, 2006, 07:16:42
Job time : 3776 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:33:20 ; Search time 282 Seconds  
(without alignments)  
1488.921 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttcccgagtgagg.....gctattattagaggagcgaa 63

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9593994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseqn 21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	13	ADT78252
2	38.4	61.0	112	13	ADT78220
3	38.4	61.0	112	13	ADT78224
4	38.4	61.0	112	13	ADT78219
5	36.6	58.1	112	13	ADT78211
6	34.8	55.2	112	13	ADT78210
7	33.6	53.3	91	9	ACC85363
8	33.6	53.3	91	10	AD834206
9	33.6	53.3	112	13	ADT78229
10	33.6	53.3	112	13	ADT78231
11	33.6	53.3	112	13	ADT78228
12	33.6	53.3	112	13	ADT78230
13	33.6	53.3	112	13	ADT78207
14	33.6	53.3	112	13	ADT78204
15	33.6	53.3	112	13	ADT78208
16	33.6	53.3	112	13	ADT78206
17	33.6	53.3	112	13	ADT78205
18	33.6	53.3	112	13	ADT78209
19	33.6	53.3	113	14	AEA36357

20	33.6	53.3	119	14	ADX17034
21	33.6	53.3	127	4	AAF84276
22	33.6	53.3	129	2	AA21430
23	33.6	53.3	140	2	AA21424
24	33.6	53.3	142	6	ABS55361
25	33.6	53.3	150	2	AA21406
26	33.6	53.3	161	2	AA21423
27	33.6	53.3	164	2	AA21431
28	33.6	53.3	165	2	AA21409
29	33.6	53.3	168	2	AA21407
30	33.6	53.3	168	3	AA288175
31	33.6	53.3	168	4	AAF25352
32	33.6	53.3	168	4	AAF57902
33	33.6	53.3	176	12	ADM01282
34	33.6	53.3	184	4	AAF89143
35	33.6	53.3	201	2	AAT66301
36	33.6	53.3	220	6	ABS54934
37	33.6	53.3	233	13	ADT78239
38	33.6	53.3	234	13	ADT78243
39	33.6	53.3	244	3	AAA47372
40	33.6	53.3	244	3	AA288176
41	33.6	53.3	244	4	AAF25353
42	33.6	53.3	244	4	AAF57903
43	33.6	53.3	258	2	AA21429
44	33.6	53.3	804	10	ADE34327
45	33.6	53.3	1134	2	AAT85195

#### ALIGNMENTS

RESULT 1

ADT78252  
ID ADT78252 standard; DNA; 63 BP.

XX AC ADT78252;

XX DT

XX 27-JAN-2005 (first entry)

XX DE Mutant Prm promoter (Prn11) useful for transgene expression in plants.

XX KW Heterologous molecule expression; plastid rRNA operon; Prm promoter;

XX KW transgenic plant; transgene expression;

XX KW Prm transcription modulating element; PTME; chimeric promoter; mutant;

XX ds.

XX Synthetic.

OS Unidentified.

XX US2004221338-A1.

XX PD 04-NOV-2004.

XX PF 15-DEC-2003; 2003US-00737251.

XX PR 13-DEC-2002; 2002US-0433302P.

XX PA (MALI/) MALIGA P.

XX PA (SUZU/) SUZUKI J Y.

XX PI Maliga P, Suzuki JY;

XX DR WPI; 2004-774976/76.

XX PT New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

XX PS Claim 7; SEQ ID NO 51; 34pp; English.

XX CC The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prm) sequences

CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this  
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
 CC of higher plants, comprising at least one Prn transcription modulating  
 CC element (PTME) operably linked to a promoter element, the chimeric  
 CC promoter being further operably linked to a sequence encoding a  
 CC heterologous molecule of interest, and (d) a vector comprising the  
 CC chimeric promoter. The nucleic acid sequence is operably linked to a  
 CC sequence encoding a heterologous molecule of interest or its precursor.  
 CC Expression of the heterologous molecule is decreased or increased  
 CC relative to that observed using wild-type Prn sequence. The nucleic acid  
 CC sequence is useful for constructing chimeric promoters for transgene  
 CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a mutant Prn promoter that  
 CC can be used to express heterologous molecules in the plastids of higher  
 CC plants.  
 XX  
 SQ Sequence 63 BP; 13 A; 12 C; 24 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 13; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-14;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCTTCTCCGAGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATTATAGAGGAGC 60  
 DB 1 GAGCTTCTCCGAGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATTATAGAGGAGC 60

QY 61 GAA 63  
 DB 61 GAA 63

RESULT 2  
 ADT78220  
 ID ADT78220 standard; DNA; 112 BP.  
 XX  
 AC ADT78220;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE DNA sequence of Prn promoter derivative pJYS172.  
 XX  
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004221338-Al.  
 XX  
 PD 04-NOV-2004.  
 XX  
 PF 15-DEC-2003; 2003US-00737251.  
 XX  
 PR 13-DEC-2002; 2002US-0433302P.  
 XX  
 PA (MALI/) MALIGA P.  
 PA (SUZU/) SUZUKI J Y.  
 PI Maliga P, Suzuki JY;  
 XX  
 DR WPI; 2004-774976/76.  
 XX  
 PS New isolated nucleic acid sequence, useful for promoting expression of  
 PT heterologous molecules in the plastids of higher plants and for  
 PT constructing chimeric promoters for transgene expression.  
 XX  
 PS Claim 1; SEQ ID NO 19; 34pp; English.  
 XX  
 CC The invention relates to nucleic acid sequences for promoting expression  
 CC of heterologous molecules in the plastids of higher plants. The nucleic

CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this  
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
 CC of higher plants, comprising at least one Prn transcription modulating  
 CC element (PTME) operably linked to a promoter element, the chimeric  
 CC promoter being further operably linked to a sequence encoding a  
 CC heterologous molecule of interest, and (d) a vector comprising the  
 CC chimeric promoter. The nucleic acid sequence is operably linked to a  
 CC sequence encoding a heterologous molecule of interest or its precursor.  
 CC Expression of the heterologous molecule is decreased or increased  
 CC relative to that observed using wild-type Prn sequence. The nucleic acid  
 CC sequence is useful for constructing chimeric promoters for transgene  
 CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a Prn promoter derivative.  
 XX  
 SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;  
 Best Local Similarity 87.5%; Pred. No. 0.00016;  
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 16 GTGGATTGACCTGAGGGGGCTCCCTAGGCTATTATAGAGGAGCGAA 63  
 DB 28 GTGGATTGACCTGAGGGGGCAGGCTAGGCTATTATTCCTGGAGCGAA 75

RESULT 3  
 ADT78224  
 ID ADT78224 standard; DNA; 112 BP.  
 XX  
 AC ADT78224;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE DNA sequence of Prn promoter derivative pJYS176.  
 XX  
 KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004221338-Al.  
 XX  
 PD 04-NOV-2004.  
 XX  
 PF 15-DEC-2003; 2003US-00737251.  
 XX  
 PR 13-DEC-2002; 2002US-0433302P.  
 XX  
 PA (MALI/) MALIGA P.  
 PA (SUZU/) SUZUKI J Y.  
 PI Maliga P, Suzuki JY;  
 XX  
 DR WPI; 2004-774976/76.  
 XX  
 PS New isolated nucleic acid sequence, useful for promoting expression of  
 PT heterologous molecules in the plastids of higher plants and for  
 PT constructing chimeric promoters for transgene expression.  
 XX  
 PS Claim 1; SEQ ID NO 23; 34pp; English.

CC The invention relates to nucleic acid sequences for promoting expression  
 CC of heterologous molecules in the plastids of higher plants. The nucleic  
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this

vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prn promoter element, the chimeric element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prn promoter derivative.

Sequence 112 BP; 33 A; 16 C; 42 G; 21 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
|||||  
Db 28 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 75  
|||||

## RESULT 4

ADT78219  
ID ADT78219 standard; DNA; 112 BP.

AC ADT78219;

DT 27-JAN-2005 (first entry)

DE DNA sequence of Prn promoter derivative pJYS171.

XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
KW transgenic plant; transgene expression;  
KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
XX Unidentified.

XX US2004221338-A1.

XX 04-NOV-2004.

XX 15-DEC-2003; 2003US-00737251.

XX 13-DEC-2002; 2002US-0433302P.

XX (MALI/) MALIGA P.  
XX (SUZU/) SUZUKI J Y.

XX Maliga P, Suzuki JY;

XX WPI; 2004-774976/76.

XX New isolated nucleic acid sequence, useful for promoting expression of  
PT heterologous molecules in the plastids of higher plants and for  
PT constructing chimeric promoters for transgene expression.

XX Claim 1; SEQ ID NO 18; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression  
CC of heterologous molecules in the plastids of higher plants. The nucleic  
CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
CC mutations which minimise homologous recombination at the Prn operon  
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
CC nucleic acid sequence above, (b) a transgenic plant comprising this  
CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
CC of higher plants, comprising at least one Prn promoter element, the chimeric  
CC element (PTME) operably linked to a promoter element, the chimeric  
CC promoter being further operably linked to a sequence encoding a  
CC heterologous molecule of interest, and (d) a vector comprising the

CC chimeric promoter. The nucleic acid sequence is operably linked to a  
CC sequence encoding a heterologous molecule of interest or its precursor.  
CC Expression of the heterologous molecule is decreased or increased  
CC relative to that observed using wild-type Prn sequence. The nucleic acid  
CC sequence is useful for constructing chimeric promoters for transgene  
CC expression and for driving high level expression of heterologous proteins  
CC in plastids. The present sequence represents a Prn promoter derivative.

XX Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
|||||  
Db 28 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 75  
|||||

## RESULT 5

ADT78211  
ID ADT78211 standard; DNA; 112 BP.

XX ADT78211;

XX 27-JAN-2005 (first entry)

DE DNA sequence of Prn promoter derivative pJYS119.

XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
KW transgenic plant; transgene expression;  
KW Prn transcription modulating element; PTME; chimeric promoter; ds.

XX Unidentified.

XX US2004221338-A1.

XX 04-NOV-2004.

XX 15-DEC-2003; 2003US-00737251.

XX 13-DEC-2002; 2002US-0433302P.

XX (MALI/) MALIGA P.  
XX (SUZU/) SUZUKI J Y.

XX Maliga P, Suzuki JY;

XX WPI; 2004-774976/76.

XX New isolated nucleic acid sequence, useful for promoting expression of  
PT heterologous molecules in the plastids of higher plants and for  
PT constructing chimeric promoters for transgene expression.

XX Claim 1; SEQ ID NO 10; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression  
CC of heterologous molecules in the plastids of higher plants. The nucleic  
CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
CC mutations which minimise homologous recombination at the Prn operon  
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
CC nucleic acid sequence above, (b) a transgenic plant comprising this  
CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
CC of higher plants, comprising at least one Prn promoter element, the chimeric  
CC element (PTME) operably linked to a promoter element, the chimeric  
CC promoter being further operably linked to a sequence encoding a  
CC heterologous molecule of interest, and (d) a vector comprising the  
CC chimeric promoter. The nucleic acid sequence is operably linked to a  
CC sequence encoding a heterologous molecule of interest or its precursor.  
CC Expression of the heterologous molecule is decreased or increased  
CC relative to that observed using wild-type Prn sequence. The nucleic acid  
CC sequence is useful for constructing chimeric promoters for transgene

CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a Prn promoter derivative.

XX Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;

Query Match 58.1%; Score 36.6; DB 13; Length 112;  
 Best Local Similarity 82.4%; Pred. No. 0.00074;  
 Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 13 GAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 DB 25 GAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGAGCGAA 75  
 |||||

## RESULT 6

ADT78210  
 ID ADT78210 standard; DNA; 112 BP.

AC ADT78210;

DT 27-JAN-2005 (first entry)

XX DNA sequence of Prn promoter derivative pJYS118.

DE Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression;  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.

XX Unidentified.

OS US2004221338-A1.

XX 04-NOV-2004.

PF 15-DEC-2003; 2003US-00737251.

XX 13-DEC-2002; 2002US-0433302P.

PR (MALI/) MALIGA P.

PA (SUZU/) SUZUKI J Y.

XX Maliga P, Suzuki JY;

PI WPI; 2004-774976/76.

DR New isolated nucleic acid sequence, useful for promoting expression of  
 XX heterologous molecules in the plastids of higher plants and for  
 PT constructing chimeric promoters for transgene expression.

XX Claim 1; SEQ ID NO 9; 34pp; English.

CC The invention relates to nucleic acid sequences for promoting expression  
 CC of heterologous molecules in the plastids of higher plants. The nucleic  
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this  
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
 CC of higher plants, comprising at least one Prn transcription modulating  
 CC element (PTME) operably linked to a promoter element, the chimeric  
 CC promoter being further operably linked to a sequence encoding a  
 CC heterologous molecule of interest, and (d) a vector comprising the  
 CC chimeric promoter. The nucleic acid sequence is operably linked to a  
 CC sequence encoding a heterologous molecule of interest or its precursor.  
 CC Expression of the heterologous molecule is decreased or increased  
 CC relative to that observed using wild-type Prn sequence. The nucleic acid  
 CC sequence is useful for constructing chimeric promoters for transgene  
 CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a Prn promoter derivative.

XX Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;

Query Match 55.2%; Score 34.8; DB 13; Length 112;  
 Best Local Similarity 77.8%; Pred. No. 0.0035;  
 Matches 42; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 10 TCCGAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 DB 22 TCCCTCGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGAGCGAA 75  
 |||||

## RESULT 7

ACC85363  
 ID ACC85363 standard; DNA; 91 BP.

XX ACC85363;

DT 18-SEP-2003 (first entry)

DE N tabacum Prn16 promoter.

XX Vegetable plastid transformation; transgenic; recognition sequence;  
 KW plant; site-specific integration; nutrition; seed production; gene;  
 KW chemical production; promoter; ds.

XX Nicotiana tabacum.

XX WO2003054201-A1.

XX 03-JUL-2003.

XX 16-DEC-2002; 2002WO-EP014303.

XX 20-DEC-2001; 2001DE-01063159.

XX (SUNG-) SUNGENE GMBH & CO KGAA.

XX Biesgen C;

XX WPI; 2003-541820/51.

DR Site-specific integration of DNA into plastid DNA, useful for making  
 XX transgenic plants used e.g. as food, by recombinase-mediated insertion.

PS Disclosure; Page 132; 164pp; German.

XX The present invention relates to a method for the site-specific  
 CC integration of a DNA sequence into the plastid DNA of a plant or its  
 CC derived cells. Transgenic plants in which a DNA sequence has been  
 CC integrated, also their cell cultures, organs, tissues etc. are useful in  
 CC human or animal nutrition, to produce seeds, and to produce  
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,  
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The  
 CC present sequence is a gene fragment shown in the exemplification of the  
 CC invention

XX Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;

Query Match 53.3%; Score 33.6; DB 9; Length 91;  
 Best Local Similarity 81.2%; Pred. No. 0.0096;  
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 |||||  
 DB 34 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTCTGGAGCGAA 81  
 |||||

## RESULT 8

ADE34206

ID ADE34206 standard; DNA; 91 BP.

XX ADE34206;

XX 29-JAN-2004 (first entry)

DE XX Tobacco Prn16 promoter DNA.

KW XX plastid; plant; homotransplastomic cell; insertion sequence; nutrition;

KW XX seed production; enzyme; vitamin; amino acid; flavouring;

KW XX aromatising agent; dye; antibody; vaccine; ds.

XX XX Nicotiana tabacum.

XX XX WO2003054189-A2.

XX XX 03-JUL-2003.

XX XX 16-DEC-2002; 2002WO-EP014302.

XX XX 20-DEC-2001; 2001DE-01063161.

XX XX (SUNG-) SUNGENE GMBH & CO KGAA.

XX XX Biesgen C;

XX XX WPI; 2003-541816/51.

XX XX Method for integrating DNA into plant plastids, useful for making

PT transgenic plants for e.g. food or animal feed, by inducing targeted

PT double-strand DNA breaks.

XX XX Disclosure; SEQ ID NO 46; 182pp; German.

XX XX This invention describes a novel method for integrating a DNA sequence

CC into the plastid DNA of a multicellular plant or its derived cells and

CC for selecting homotransplastomic cells or plants. The method comprises

CC inducing DNA double-strand breaks in plant plastid DNA, which contains at

CC least one recognition site for targeted induction of such breaks, by

CC treating the plant or its cells with an enzyme able to create these

CC breaks and a transformation construct that contains an insertion sequence

CC which is inserted into the plastid DNA so that the function of the

CC recognition site for targeted induction of breaks is inactivated, i.e. it

CC is no longer cleaved by the enzyme. Plants or cells in which the

CC insertion sequence has been inserted are then selected. Transgenic plants

CC in which the DNA sequence has been integrated, and also their cell

CC cultures, organs, tissues, are useful in human or animal nutrition, for

CC producing seeds, and pharmaceuticals or fine chemicals, e.g. enzymes,

CC vitamins, amino acids, flavourings and aromatising agents, dyes,

CC antibiotics and vaccines. The method eliminates the need for

CC antibiotic/herbicide selection markers and ensures efficient integration

CC of foreign DNA into all copies of plastid DNA, also effective selection,

CC so provides a quicker, more efficient and less expensive method of

CC producing homotransplastomic plants. The genetic constructs used are

CC small, since only short homology regions are required. Double-crossover

CC events occur easily in plastid DNA, at specific locations, avoiding the

CC problems of gene silencing associated with recombination in the nucleus

CC and high level expression can be achieved, because of the high copy

CC number of plastid DNA. Foreign DNA will not be transferred in pollen

CC (inheritance of plastid DNA is maternal) and since plastids resemble

CC prokaryotes, they can express several genes from polycistronic operons,

XX under control of a single promoter.

XX XX Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;

SQ Query Match 53.3%; Score 33.6; DB 10; Length 91;

Best Local Similarity 81.2%; Pred. No. 0.0096;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

DB 34 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTGGAGCGAA 81

RESULT 9

ADT78229

ID ADT78229 standard; DNA; 112 BP.

XX XX

AC ADT78229;

XX 27-JAN-2005 (first entry)

XX DNA sequence of Prn promoter derivative pJYS183.

XX XX

XX 27-JAN-2005 (first entry)

XX DNA sequence of Prn promoter derivative pJYS181.

XX XX

XX DNA sequence of Prn promoter derivative pJYS181.

XX XX

XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;

KW transgenic plant; transgene expression;

KW Prn transcription modulating element; PTME; chimeric promoter; ds.

XX OS Unidentified.

XX XX US2004221338-A1.

XX XX 04-NOV-2004.

XX XX 15-DEC-2003; 2003US-00737251.

XX XX 13-DEC-2002; 2002US-0433302P.

XX XX (MALI/) MALIGA P.

XX XX (SUZU/) SUZUKI J Y.

XX XX Maliga P, Suzuki JY;

XX XX WPI; 2004-774976/76.

XX XX New isolated nucleic acid sequence, useful for promoting expression of

PT heterologous molecules in the plastids of higher plants and for

PT constructing chimeric promoters for transgene expression.

XX XX Claim 1; SEQ ID NO 28; 34pp; English.

XX XX The invention relates to nucleic acid sequences for promoting expression

CC of heterologous molecules in the plastids of higher plants. The nucleic

CC acid sequences are selected from plastid rRNA operon (Prn) sequences

CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise

CC mutations which minimise homologous recombination at the Prn operon

CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the

CC nucleic acid sequence above, (b) a transgenic plant comprising this

CC vector, (c) a chimeric promoter for expression of transgenes in plastids

CC of higher plants, comprising at least one Prn transcription modulating

CC element (PTME) operably linked to a promoter element, the chimeric

CC promoter being further operably linked to a sequence encoding a

CC heterologous molecule of interest, and (d) a vector comprising the

CC chimeric promoter. The nucleic acid sequence is operably linked to a

CC sequence encoding a heterologous molecule of interest or its precursor.

CC Expression of the heterologous molecule is decreased or increased

CC relative to that observed using wild-type Prn sequence. The nucleic acid

CC sequence is useful for constructing chimeric promoters for transgene

CC expression and for driving high level expression of heterologous proteins

CC in plastids. The present sequence represents a Prn promoter derivative.

XX XX Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

SQ Query Match 53.3%; Score 33.6; DB 13; Length 112;

Best Local Similarity 81.2%; Pred. No. 0.01;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTGGAGCGAA 75

RESULT 10

ADT78231

ID ADT78231 standard; DNA; 112 BP.

XX XX

AC ADT78231;

XX XX

DT 27-JAN-2005 (first entry)

XX XX

DE DNA sequence of Prn promoter derivative pJYS183.

XX XX

KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
 XX Unidentified.  
 XX US2004221338-A1.  
 XX 04-NOV-2004.  
 XX 15-DEC-2003; 2003US-00737251.  
 XX 13-DEC-2002; 2002US-0433302P.  
 XX (MALI/) MALIGA P.  
 XX (SUZU/) SUZUKI J Y.  
 XX Maliga P, Suzuki JY;  
 XX WPI; 2004-774976/76.  
 XX New isolated nucleic acid sequence, useful for promoting expression of  
 PT heterologous molecules in the plastids of higher plants and for  
 PT constructing chimeric promoters for transgene expression.  
 XX Claim 1; SEQ ID NO 30; 34pp; English.  
 XX The invention relates to nucleic acid sequences for promoting expression  
 CC of heterologous molecules in the plastids of higher plants. The nucleic  
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this  
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
 CC of higher plants, comprising at least one Prn transcription modulating  
 CC element (PTME) operably linked to a promoter element, the chimeric  
 CC promoter being further operably linked to a sequence encoding a  
 CC heterologous molecule of interest, and (d) a vector comprising the  
 CC chimeric promoter. The nucleic acid sequence is operably linked to a  
 CC sequence encoding a heterologous molecule of interest or increased  
 CC expression of the heterologous molecule is decreased or increased  
 CC relative to that observed using wild-type Prn sequence. The nucleic acid  
 CC sequence is useful for constructing chimeric promoters for transgene  
 CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a Prn promoter derivative.  
 XX SQ Sequence 112 BP; 30 A; 17 C; 41 G; 24 T; 0 U; 0 Other;  
 Query Match 53.3%; Score 33.6; DB 13; Length 112;  
 Best Local Similarity 81.2%; Pred. No. 0.01;  
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 Db 28 GTGGATTGACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 75  
 RESULT 11  
 ADT78228  
 ID ADT78228 standard; DNA; 112 BP.  
 XX AC ADT78228;  
 XX 27-JAN-2005 (first entry)  
 XX DNA sequence of Prn promoter derivative pJYS180.  
 XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
 XX Unidentified.

XX US2004221338-A1.  
 XX 04-NOV-2004.  
 XX 15-DEC-2003; 2003US-00737251.  
 XX 13-DEC-2002; 2002US-0433302P.  
 XX (MALI/) MALIGA P.  
 XX (SUZU/) SUZUKI J Y.  
 XX Maliga P, Suzuki JY;  
 XX WPI; 2004-774976/76.  
 XX New isolated nucleic acid sequence, useful for promoting expression of  
 PT heterologous molecules in the plastids of higher plants and for  
 PT constructing chimeric promoters for transgene expression.  
 XX Claim 1; SEQ ID NO 27; 34pp; English.  
 XX The invention relates to nucleic acid sequences for promoting expression  
 CC of heterologous molecules in the plastids of higher plants. The nucleic  
 CC acid sequences are selected from plastid rRNA operon (Prn) sequences  
 CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
 CC mutations which minimise homologous recombination at the Prn operon  
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
 CC nucleic acid sequence above, (b) a transgenic plant comprising this  
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
 CC of higher plants, comprising at least one Prn transcription modulating  
 CC element (PTME) operably linked to a promoter element, the chimeric  
 CC promoter being further operably linked to a sequence encoding a  
 CC heterologous molecule of interest, and (d) a vector comprising the  
 CC chimeric promoter. The nucleic acid sequence is operably linked to a  
 CC sequence encoding a heterologous molecule of interest or increased  
 CC expression of the heterologous molecule is decreased or increased  
 CC relative to that observed using wild-type Prn sequence. The nucleic acid  
 CC sequence is useful for constructing chimeric promoters for transgene  
 CC expression and for driving high level expression of heterologous proteins  
 CC in plastids. The present sequence represents a Prn promoter derivative.  
 XX SQ Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;  
 Query Match 53.3%; Score 33.6; DB 13; Length 112;  
 Best Local Similarity 81.2%; Pred. No. 0.01;  
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 16 GTGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
 Db 28 GTGGATTGACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 75  
 RESULT 12  
 ADT78230  
 ID ADT78230 standard; DNA; 112 BP.  
 XX AC ADT78230;  
 XX 27-JAN-2005 (first entry)  
 XX DNA sequence of Prn promoter derivative pJYS182.  
 XX Heterologous molecule expression; plastid rRNA operon; Prn promoter;  
 KW transgenic plant; transgene expression;  
 KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
 XX Unidentified.  
 XX US2004221338-A1.  
 XX 04-NOV-2004.

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PF 15-DEC-2003; 2003US-00737251.
PR 13-DEC-2002; 2002US-0433302P.
XX (MALI/) MALIGA P.
XX (SUZU/) SUZUKI J Y.
XX Maliga P, Suzuki JY;
XX WPI; 2004-774976/76.
XX New isolated nucleic acid sequence, useful for promoting expression of
XX heterologous molecules in the plastids of higher plants and for
XX constructing chimeric promoters for transgene expression.
XX Claim 1; SEQ ID NO 29; 34pp; English.
XX The invention relates to nucleic acid sequences for promoting expression
XX of heterologous molecules in the plastids of higher plants. The nucleic
XX acid sequences are selected from plastid rRNA operon (Prn) sequences
XX given as SEQ ID Nos: 4-30 in the specification, or which may comprise
XX mutations which minimise homologous recombination at the Prn operon
XX (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
XX nucleic acid sequence above, (b) a transgenic plant comprising this
XX vector, (c) a chimeric promoter for expression of transgenes in plastids
XX of higher plants, comprising at least one Prn transcription modulating
XX element (PTME) operably linked to a promoter element, the chimeric
XX heterologous molecule of interest, and (d) a vector comprising the
XX chimeric promoter. The nucleic acid sequence is operably linked to a
XX sequence encoding a heterologous molecule of interest or its precursor.
XX Expression of the heterologous molecule is decreased or increased
XX relative to that observed using wild-type Prn sequence. The nucleic acid
XX sequence is useful for constructing chimeric promoters for transgene
XX expression and for driving high level expression of heterologous proteins
XX in plastids. The present sequence represents a Prn promoter derivative.
XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

Query Match 53.3%; Score 33.6; DB 13; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGACGAA 63
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGACCGAA 75

RESULT 13
ADT78207
ID ADT78207 standard; DNA; 112 BP.
XX AC ADT78207;
XX DT 27-JAN-2005 (first entry)
XX DE DNA sequence of Prn promoter derivative pUYS115.
XX KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
XX transgenic plant; transgene expression;
XX Prn transcription modulating element; PTME; chimeric promoter; ds.
XX OS Unidentified.
XX PN US2004221338-A1.
XX PD 04-NOV-2004.
XX PF 15-DEC-2003; 2003US-00737251.
XX PR 13-DEC-2002; 2002US-0433302P.
XX (MALI/) MALIGA P.
XX (SUZU/) SUZUKI J Y.
XX Maliga P, Suzuki JY;
XX WPI; 2004-774976/76.

Query Match 53.3%; Score 33.6; DB 13; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGACGAA 63
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGACCGAA 75

RESULT 14
ADT78204
ID ADT78204 standard; DNA; 112 BP.
XX AC ADT78204;
XX DT 27-JAN-2005 (first entry)
XX DE DNA sequence of Prn promoter derivative pUYS112.
XX KW Heterologous molecule expression; plastid rRNA operon; Prn promoter;
XX transgenic plant; transgene expression;
XX Prn transcription modulating element; PTME; chimeric promoter; ds.
XX OS Unidentified.
XX PN US2004221338-A1.
XX PD 04-NOV-2004.
XX PF 15-DEC-2003; 2003US-00737251.
XX PR 13-DEC-2002; 2002US-0433302P.
XX (MALI/) MALIGA P.
XX (SUZU/) SUZUKI J Y.
XX Maliga P, Suzuki JY;
XX WPI; 2004-774976/76.

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XX New isolated nucleic acid sequence, useful for promoting expression of  
PT heterologous molecules in the plastids of higher plants and for  
PT constructing chimeric promoters for transgene expression.  
PS Disclosure; SEQ ID NO 3; 34pp; English.  
XX  
CC The invention relates to nucleic acid sequences for promoting expression  
CC of heterologous molecules in the plastids of higher plants. The nucleic  
CC acid sequences are selected from plastid RNA operon (Prn) sequences  
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
CC mutations which minimise homologous recombination at the Prn operon  
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
CC nucleic acid sequence above, (b) a transgenic plant comprising this  
CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
CC of higher plants, comprising at least one Prn transcription modulating  
CC element (PTME) operably linked to a promoter element, the chimeric  
CC promoter being further operably linked to a sequence encoding a  
CC heterologous molecule of interest, and (d) a vector comprising the  
CC chimeric promoter. The nucleic acid sequence is operably linked to a  
CC sequence encoding a heterologous molecule of interest or its precursor.  
CC Expression of the heterologous molecule is decreased or increased  
CC relative to that observed using wild-type Prn sequence. The nucleic acid  
CC sequence is useful for constructing chimeric promoters for transgene  
CC expression and for driving high level expression of heterologous proteins  
CC in plastids. The present sequence represents a Prn promoter derivative.  
XX  
SQ Sequence 112 BP; 31 A; 17 C; 41 G; 23 T; 0 U; 0 Other;  
Query Match 53.3%; Score 33.6; DB 13; Length 112;  
Best Local Similarity 81.2%; Pred. No. 0.01;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTTGGGAGCGAA 75  
RESULT 15  
ADT78208  
ID ADT78208 standard; DNA; 112 BP.  
XX  
AC ADT78208;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE DNA sequence of Prn promoter derivative pJVS116.  
XX  
KW Heterologous molecule expression; plastid RNA operon; Prn promoter;  
KW transgenic plant; transgene expression;  
KW Prn transcription modulating element; PTME; chimeric promoter; ds.  
XX  
OS Unidentified.  
XX  
XX US2004221338-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 15-DEC-2003; 2003US-00737251.  
XX  
PR 13-DEC-2002; 2002US-0433302P.  
XX  
PA (MALI/) MALIGA P.  
PA (SUZU/) SUZUKI J Y.  
XX  
PI Maliga P, Suzuki JY;  
XX  
DR WPI; 2004-774976/76.  
XX  
PT New isolated nucleic acid sequence, useful for promoting expression of  
PT heterologous molecules in the plastids of higher plants and for  
PT constructing chimeric promoters for transgene expression.  
XX

PS Claim 1; SEQ ID NO 7; 34pp; English.  
XX  
CC The invention relates to nucleic acid sequences for promoting expression  
CC of heterologous molecules in the plastids of higher plants. The nucleic  
CC acid sequences are selected from plastid RNA operon (Prn) sequences  
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise  
CC mutations which minimise homologous recombination at the Prn operon  
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the  
CC nucleic acid sequence above, (b) a transgenic plant comprising this  
CC vector, (c) a chimeric promoter for expression of transgenes in plastids  
CC of higher plants, comprising at least one Prn transcription modulating  
CC element (PTME) operably linked to a promoter element, the chimeric  
CC promoter being further operably linked to a sequence encoding a  
CC heterologous molecule of interest, and (d) a vector comprising the  
CC chimeric promoter. The nucleic acid sequence is operably linked to a  
CC sequence encoding a heterologous molecule of interest or its precursor.  
CC Expression of the heterologous molecule is decreased or increased  
CC relative to that observed using wild-type Prn sequence. The nucleic acid  
CC sequence is useful for constructing chimeric promoters for transgene  
CC expression and for driving high level expression of heterologous proteins  
CC in plastids. The present sequence represents a Prn promoter derivative.  
XX  
SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;  
Query Match 53.3%; Score 33.6; DB 13; Length 112;  
Best Local Similarity 81.2%; Pred. No. 0.01;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
DB 28 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTTGGGAGCGAA 75  
Search completed: February 21, 2006, 05:38:11  
Job time : 283 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:35:59 ; Search time 2168 Seconds  
(without alignments)  
1651.816 Million cell updates/sec

Title: US-10-737-251-51  
Perfect score: 63  
Sequence: 1 gagctctctccagggtggg.....gctatatagaggagcgaa 63

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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2: gb\_in.\*  
3: gb\_env.\*  
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6: gb\_pat.\*  
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9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	91	6	AX798146
2	33.6	53.3	91	6	AX798954
3	33.6	53.3	113	6	CS114516
4	33.6	53.3	119	15	CS001461
5	33.6	53.3	127	6	ES1179
6	33.6	53.3	127	6	ES1197
7	33.6	53.3	127	6	AR399398
8	33.6	53.3	127	6	AX137514
9	33.6	53.3	142	6	BD174932
10	33.6	53.3	168	6	AX076661
11	33.6	53.3	176	6	CQ797808
12	33.6	53.3	184	6	AR145914
13	33.6	53.3	201	6	AR242682
14	33.6	53.3	202	6	AR568182
15	33.6	53.3	202	6	AX076662
16	33.6	53.3	202	6	AX319835
17	33.6	53.3	210	15	AF189150
18	33.6	53.3	220	6	BD180933

19	33.6	53.3	220	6	AX537601
20	33.6	53.3	244	6	BD247598
21	33.6	53.3	244	6	AR568183
22	33.6	53.3	244	6	AX319836
23	33.6	53.3	300	6	AR171710
24	33.6	53.3	300	6	AR171711
25	33.6	53.3	553	6	CQ828073
26	33.6	53.3	557	15	DCCLGTRV
27	33.6	53.3	762	15	CPHATV
28	33.6	53.3	804	6	AX798912
29	33.6	53.3	1143	6	AR368829
30	33.6	53.3	1148	6	CQ830289
31	33.6	53.3	1183	6	BD235370
32	33.6	53.3	1293	6	CQ793220
33	33.6	53.3	1293	6	CS039141
34	33.6	53.3	1327	6	CQ828069
35	33.6	53.3	1330	6	CQ828070
36	33.6	53.3	1332	6	CQ830287
37	33.6	53.3	1359	6	AX798126
38	33.6	53.3	1359	6	AX798910
39	33.6	53.3	1417	6	AR368830
40	33.6	53.3	1487	6	CQ828074
41	33.6	53.3	1613	6	CQ830293
42	33.6	53.3	1694	6	CQ828072
43	33.6	53.3	1746	6	CQ828071
44	33.6	53.3	2113	15	CHNTRN1
45	33.6	53.3	2191	15	CRE278626

## ALIGNMENTS

RESULT 1  
AX798146  
LOCUS AX798146  
DEFINITION Sequence 22 from Patent WO03054201.  
ACCESSION AX798146  
VERSION AX798146.1 GI:37604427  
KEYWORDS  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum

REFERENCE 1  
AUTHORS Biesgen,C.  
TITLE Method for the transformation of vegetable plastids  
JOURNAL Patent: WO 03054201-A 22 03-JUL-2003;  
Sungene GmbH & Co. KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..91  
/organism="Nicotiana tabacum"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4097"  
promoter 1..91  
/note="plastidic promoter Prn16"

linear PAT 08-OCT-2003

Query Match 53.3%; Score 33.6; DB 6; Length 91;  
Best Local Similarity 81.2%; Pred. No. 0.097;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
Db 34 GTGGGATTGACGTGAGGGGCGAGGATGGCTATATTCTGGGAGCGAA 81

## RESULT 2

AX798954  
LOCUS AX798954  
DEFINITION Sequence 46 from Patent WO03054189.  
ACCESSION AX798954  
VERSION AX798954.1 GI:37605006

linear PAT 08-OCT-2003

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KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS Biesgen, C.
TITLE Methods for the transformation of vegetal plastids
JOURNAL Patent: WO 03054189-A 46 03-JUL-2003;
          Sungene GmbH & Co. KGAA (DE)
FEATURES
source 1..91
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promoter 1..91
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Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTCACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 34 GTGGGATTCACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 81

RESULT 3
LOCUS CS114516 113 bp DNA linear PAT 24-JUN-2005
DEFINITION Sequence 13 from Patent WO2005054481.
ACCESSION CS114516
VERSION CS114516.1 GI:68226041
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
AUTHORS Muehlbauer, S.
TITLE Controlling gene expression in plastids
JOURNAL Patent: WO 2005054481-A 13 16-JUN-2005;
          Icon Genetics AG (DE)
FEATURES
source 1..113
          /organism="synthetic construct"
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          /note="cloning oligo"
ORIGIN
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Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTCACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 38 GTGGGATTCACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 85

RESULT 4
LOCUS CS001461 119 bp DNA linear PLN 01-FEB-2005
DEFINITION Sequence 6 from Patent WO2005005643.
ACCESSION CS001461
VERSION CS001461.1 GI:58423938
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          asterids; lamids; Solanales; Solanaceae; Nicotiana.

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REFERENCE
AUTHORS Cox, K.M. and Peele, C.G.
TITLE Chloroplast transformation of duckweed
JOURNAL Patent: WO 2005005643-A 20-JAN-2005;
          Biolex, Inc. (US)
FEATURES
source 1..119
          /organism="Nicotiana tabacum"
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Query Match 53.3%; Score 33.6; DB 15; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTCACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 41 GTGGGATTCACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 88

RESULT 5
LOCUS E51179 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION E51179
VERSION E51179.1 GI:18629496
KEYWORDS JP 2001046073-A/16.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          asterids; lamids; Solanales; Solanaceae; Nicotiana.
          1 (bases 1 to 127)
REFERENCE
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Method for transforming plant and transformed plant
JOURNAL Patent: JP 2001046073-A 16 20-FEB-2001;
          RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT OS Nicotiana tabacum (tobacco)
          PN JP 2001046073-A/16
          PD 20-FEB-2001
          PF 09-AUG-1999 JP 1999225832
          PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
          PI C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC
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Best Local Similarity 81.2%; Pred. No. 0.097;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTCACGTGAGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63
Db 53 GTGGGATTCACGTGAGGGGCGAGGATGCTATATTCTGGGAGCGAA 100

RESULT 6
LOCUS E51197 127 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing polyester.
ACCESSION E51197
VERSION E51197.1 GI:18629514
KEYWORDS JP 2001046074-A/16.

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SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
TITLE 1 (bases 1 to 127)  
JOURNAL Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.  
PROCESS for producing polyester  
PATENT: JP 2001046074-A 16 20-FEB-2001;  
RIKAGAKU KENKYUSHO

COMMENT  
OS Nicotiana tabacum (tobacco)  
PN JP 2001046074-A/16  
PD 20-FEB-2001  
PF 09-AUG-1999 JP 1999225839  
PR  
PI HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIOHARU DOI  
PC C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC  
CC C12N15/00, C12N5/00

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Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
Db 53 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGAGCGAA 100

RESULT 7  
AR399398  
LOCUS AR399398 127 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6620601.  
ACCESSION AR399398  
VERSION AR399398.1 GI:40141264  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 127)  
AUTHORS Yamaguchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.  
TITLE Methods for transformation of plants, transformed plants and processes for preparation of polyesters  
JOURNAL Patent: US 6620601-A 16 16-SEP-2003;  
Riken; Saitama;  
JPX;

FEATURES  
source FH Key Location/Qualifiers  
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ORIGIN  
Query Match 53.3%; Score 33.6; DB 6; Length 127;  
Best Local Similarity 81.2%; Pred. No. 0.097;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 53 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGAGCGAA 100

RESULT 8  
AX137514  
LOCUS AX137514 127 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 16 from Patent EP1076095.  
ACCESSION AX137514  
VERSION AX137514.1 GI:14273708  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1  
Yamaguchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.  
Methods for transformation of plants, transformed plants and processes for preparation of polyesters  
PATENT: EP 1076095-A 16 14-FEB-2001;  
Riken (JP)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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ORIGIN  
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Best Local Similarity 81.2%; Pred. No. 0.097;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 53 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGAGCGAA 100

RESULT 9  
BD174932  
LOCUS BD174932 142 bp DNA linear PAT 18-MAR-2003  
DEFINITION A system for expressing protein using plants.  
ACCESSION BD174932  
VERSION BD174932.1 GI:29120626  
KEYWORDS JP 2002272476-A/2.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 142)  
Tomizawa, K. and Yokota, A.  
A system for expressing protein using plants  
PATENT: JP 2002272476-A 2 24-SEP-2002;  
RESEARCH INSTITUTE OF INNOVATIVE TECHNOLOGY FOR THE EARTH  
OS Nicotiana tabacum (tobacco)  
PN JP 2002272476-A/2  
PD 24-SEP-2002  
PP 22-MAR-2001 JP 2001083569  
PI KENICHI TOMIZAWA, AKIHO YOKOTA  
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, C12N15/00, C12N5/00 CC  
rrn promoter  
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Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 53 GTGGGATTGACGTGAGGGGGCAGGGATGGCTATATTCTCGGAGCGAA 100

RESULT 10  
AX076661  
LOCUS AX076661 168 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 1 from Patent WO0104331.  
ACCESSION AX076661  
VERSION AX076661.1 GI:127111193  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1  
AUTHORS Staub, J.M.  
TITLE Enhanced expression of proteins using gfp  
JOURNAL Patent: WO 0104331-A 1 18-JAN-2001;  
Calgene LLC (US)  
FEATURES  
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Db 63 GTGGGATTGACGTAGGGGGCGAGGATGGCTATATTCTGGAGCGAA 110  
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CQ797808  
LOCUS CQ797808 176 bp DNA linear PAT 20-APR-2004  
DEFINITION Sequence 14 from Patent WO2004029256.  
ACCESSION CQ797808  
VERSION CQ797808.1 GI:46426081  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS selman-housein Sosa, G., aguiar Cabeza, E., gonz lez Quintero, A.D.  
and ramos gonz lez, O.  
TITLE Vector for the production of transplastomic angiosperm plants  
JOURNAL Patent: WO 2004029256-A 14 08-APR-2004;  
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)  
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/note="Description of Artificial Sequence: Synthetic DNA  
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Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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Db 56 GTGGGATTGACGTAGGGGGCGAGGATGGCTATATTCTGGAGCGAA 103  
RESULT 12  
AR145914  
LOCUS AR145914 184 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 3 from patent US 6218145.  
ACCESSION AR145914  
VERSION AR145914.1 GI:15109103

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 184)  
AUTHORS Bogosian, G., O'Neil, J.P. and Staub, J.M.  
TITLE Bacterial expression systems based on plastic or mitochondrial  
promoter combinations  
JOURNAL Patent: US 6218145-A 3 17-APR-2001;  
FEATURES  
source Location/Qualifiers  
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RESULT 13  
AR242682  
LOCUS AR242682 201 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 58 from patent US 6472586.  
ACCESSION AR242682  
VERSION AR242682.1 GI:27289157  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 201)  
AUTHORS Maliga, P., Allison, L.A. and Hajdukiewicz, P.T.  
TITLE Nuclear-encoded transcription system in plastids of higher plants  
JOURNAL Patent: US 6472586-A 58 29-OCT-2002;  
Rutgers, The State University of New Jersey; Piscataway, NJ  
FEATURES  
source 1..201  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Query Match 53.3%; Score 33.6; DB 6; Length 201;  
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Db 45 GTGGGATTGACGTAGGGGGCGAGGATGGCTATATTCTGGAGCGAA 92  
RESULT 14  
AR568182  
LOCUS AR568182 202 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 1 from patent US 6781033.  
ACCESSION AR568182  
VERSION AR568182.1 GI:53986476  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 202)  
AUTHORS Staub, J.M., Ye, G. and Broyles, D.L.  
TITLE Method for the transformation of plant cell plastids  
JOURNAL Patent: US 6781033-A 1 24-AUG-2004;  
Monsanto Technology LLC; St. Louis, MO;  
WOX;  
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## ORIGIN

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## RESULT 15

AX076662  
LOCUS AX076662 202 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 2 from Patent WO0104331.

ACCESSION AX076662

VERSION AX076662.1 GI:12711194

## KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

## REFERENCE

1 Staub,J.M.

AUTHORS Enhanced expression of proteins using gfp

TITLE Patent: WO 0104331-A 2 18-JAN-2001;

JOURNAL Calgene LLC (US)

## FEATURES

source Location/Qualifiers

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/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

## ORIGIN

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Best Local Similarity 81.2%; Pred. No. 0.096;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GTGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGAGCGAA 63  
|||||  
Db 45 GTGGATTGACGTGAGGGGGCAGGATGGCTATATTTCTGGAGCGAA 92

Search completed: February 21, 2006, 06:13:36

Job time : 2171 secs